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Host-specific microbial communities in three sympatric North Sea sponges

(Article)

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Abstract

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The establishment of next-generation technology sequencing has deepened our knowledge of marine sponge-associated microbiota with the identification of at least 32 phyla of Bacteria and Archaea from a large number of sponge species. In this study, we assessed the diversity of the microbial communities hosted by three sympatric sponges living in a semi-enclosed North Sea environment using pyrosequencing of bacterial and archaeal 16S ribosomal RNA gene fragments. The three sponges harbor species-specific communities each dominated by a different class of Proteobacteria. An α -proteobacterial Rhodobacter-like phylotype was confirmed as the predominant symbiont of *Halichondria panicea*. The microbial communities of *Haliclona xena* and *H. oculata* are described for the first time in this study and are dominated by Gammaproteobacteria and Betaproteobacteria, respectively. Several common phylotypes belonging to Chlamydiae, TM6, Actinobacteria, and Betaproteobacteria were detected in all sponge samples. A number of phylotypes of the phylum Chlamydiae were present at an unprecedentedly high relative abundance of up to $14.4 \pm 1.4\%$ of the total reads, which suggests an important ecological role in North Sea sponges. These Chlamydiae-affiliated operational taxonomic units may represent novel lineages at least at the genus level as they are only 86–92% similar to known sequences. © 2014 Federation of European Microbiological Societies. Published by John Wiley & Sons Ltd.

Author keywords

Chlamydiae Proteobacteria Host-specific Microbial diversity Pyrosequencing Sponge microbiota

Indexed keywords

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bacterium detection method eukaryote host specificity identification method
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Regional Index:

Atlantic Ocean North Sea

Species Index:

Actinobacteria Archaea Bacteria (microorganisms) Betaproteobacteria Chlamydiae
Gammaproteobacteria Halichondria panicea Haliclona xena Proteobacteria Rhodobacter
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